UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/532,198	08/08/2005	Alejandro Sanchez	21101.0049U2	8394

23859 7590 12/23/2010

Ballard Spahr LLP
SUITE 1000
999 PEACHTREE STREET
ATLANTA, GA 30309-3915

EXAMINER	
HOANG, SON T	
ART UNIT	PAPER NUMBER
2165	
MAIL DATE	DELIVERY MODE
12/23/2010	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/532,198	SANCHEZ ET AL.	
	Examiner	Art Unit	
	SON T. HOANG	2165	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *03* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *02 November 2010*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *85-110 and 112* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *85-110 and 112* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *21 April 2005* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on August 11, 2010 has been entered.

Response to Amendment

2. This communication is in response to the amendment filed on April 1, 2010.

Claim 111 is canceled.

Claims 85-110, and **112** are pending.

Response to Arguments

3. Applicant's arguments with respect to the 35 U.S.C. 103(a) rejections of the pending claims have been considered but are moot in view of the new ground of rejections presented hereon.

Claim Objections

4. **Claims 83**, **94**, and **103** are objected to due to having abbreviation "mRNA" without being fined explicitly in the claimed language. Correction and/or revision are required.

Claim 85 is objected for citing "*the plurality of databases query result data*" on line 4 without corresponding antecedent basis.

Claim 87 is objected since it is not clear whether the claimed *"a user"* refers to "*a user*" in step *f* of **claim 85**.

Claim 94 is objected for citing "*the version of each…*" on line 3 and "the *plurality of databases query result data*" on line 11 without corresponding antecedent bases.

Claim 98 is objected since it is not clear whether the claimed *"a user"* refers to "*a user*" in step *k* of **claim 94**.

Claim 103 is objected for citing "*the query database node*" on lines 17-18 whilst line 13 only recites "*a query node.*"

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

5. **Claims 85-87**, and **89-93** are rejected under 35 U.S.C. 103(a) as being unpatentable by Wallace et al. (*Pat. No. US 6,920,396, filed on September 20, 2001; hereinafter Wallace*) in view of Ringwald et al. (*"GXD: a Gene Expression Database for the laboratory mouse, published in 1998, pp. 106-112; hereinafter Ringwald*), in view of Chin et al. (*Pub. No. US 2003/0054394, published on filed on August 27, 2002; hereinafter Chin*).

Regarding **claim 85**, Wallace clearly shows and discloses a method for managing a biological database (*Abstract*), comprising:

a. receiving a set of biological sequences (*A set of search query parameters specifying a plurality of sequence sets are received*, [Column 3, Lines 12-14]);

b. querying a plurality of databases with the set of biological sequences (*The structured database query is executed in a database layer. At least one queue handler loading the structured database query is provided. A plurality of biological data repositories are selected*, [Column 3, Lines 32-34]);

c. receiving from the plurality of databases query result data (*search results displayed from a search request for multiple sequence sets performed against a plurality of biological data repositories in a user interface layer*, [Column 3, Lines 24-28]) comprising expression data ([Column 3, Lines 32-34]);

d. storing the query result data in a biological database (*The relational database 33 stores tables and queues relating to search requests and results as transacted by*

the Blast Node 18, [Column 4, Lines 65-67]), wherein each sequence in the set of biological sequences is associated with a respective record comprising query result data from each of the plurality of databases (*Each biological data repository contains sequence data stored into unstructured records which are each identified by a unique identifier. The structured database query is executed against at least one database engine. The database results are obtained from the selected biological data repositories*, [Column 3, Lines 35-40]);

e. periodically performing steps b-d (*if no entries are found (block 234), the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used*, [Column 11, Lines 4-12]);

f. receiving, from a user, a request to view a record of one of the set of biological sequences (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]).

Wallace does not disclose the query result data comprising immunohistological data, in situ hybridization data, functional data, expression data, and structural data, wherein functional data comprises data that identifies a putative function, wherein expression data comprises gene expression data or mRNA expression data, wherein structural data comprises three-dimensional structural data; and displaying an executive summary of the record.

However, Ringwald discloses the result data comprising immunohistological data, *in situ* hybridization data (*the Gene Expression Data query provides access to in situ hybridization, and immunohistochmistry data*, [Page 108, Left Column, Paragraph 2]. *Figure 4 further shows query result details for RNA in situ hybridization data*, [Page 110, Figure 4's description]), and structural data comprises three-dimensional structural data (*3D graphical storage, display, and analysis of in situ expression*, [Page 106, Right Column, Lines 2-6]); and

displaying an executive summary of the record (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace for the purpose of analyzing gene expression in order to understand the function of genes and the molecular mechanisms that underlie normal development and disease.

Wallace, as modified by Ringwald, does not disclose the query result data comprising functional data, expression data, and structural data, wherein functional data comprises data that identifies a putative function, wherein expression data comprises gene expression data or mRNA expression data, wherein structural data comprises three-dimensional structural data.

However, Chin discloses the query result data comprising functional data, expression data, wherein functional data comprises data that identifies a putative

function, wherein expression data comprises gene expression data or mRNA expression data (*results of a homology search for the plurality of DNA sequences, annotative information for the plurality of DNA sequences describing the biochemical functions and physiological roles of the plurality of DNA sequences, gene expression profile data for the plurality of DNA sequences describing behavioral patterns of the plurality of DNA sequences*, [0011]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Chin with the teachings of Wallace, as modified by Ringwald, for the purpose of facilitating the identification of candidate genes from a plurality of DNA sequences for extracting and integrating information from various information sources and results of various analyses, and storing the integrated information in a form which is conducive to identification of candidate genes.

Regarding **claim 86**, Wallace further discloses the set of biological sequences comprises a nucleic acid sequence, an amino acid sequence, or a combination thereof (*Figure 4 shows for a new biological data search request, the user enters a search description 71 in a search description text box 72, followed by either a new set of FASTA formatted sequences 73 in a formatted sequence set text box 74, a local file 75 in a local file text box 76, or an existing sequence set 77 in an existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 87**, Wallace further discloses receiving the set of biological sequences comprises receiving the set of biological sequences from a user (*Figure 4*

shows for a new biological data search request, the user enters a search description 71 in a search description text box 72, followed by either a new set of FASTA formatted sequences 73 in a formatted sequence set text box 74, a local file 75 in a local file text box 76, or an existing sequence set 77 in an existing sequence set text box 78, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 89**, Wallace further discloses the plurality of databases comprises two or more databases selected from a group consisting of one or more National Center for Biotechnology Information (NCBI) databases and one or more other externally curated and maintained specialized databases (*Figure 6*).

Regarding **claim 90**, Wallace further discloses periodically performing steps b-d comprises performing steps b-d daily (*the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used,* [Column 11, Lines 4-12]).

Regarding **claim 91**, Wallace further discloses performing one or more bioinformatics functions on the set of biological sequences or the query result data (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]).

Regarding **claim 92**, Wallace further discloses the one or more bioinformatics functions comprise a sequence alignment, a gene identification, a protein identification structure prediction, a motif comparison, a biological text analysis, or a combination thereof (*The table 101 is necessary to display the individual results based on the*

specified database and requesting sequence, as each search can include multiple sequences and multiple databases., [Column 8, Lines 35-45]).

Regarding **claim 93**, Ringwald further discloses displaying an executive summary of the record comprises formatting the requested record for output to the user (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace, and Chin, for the purpose of analyzing gene expression in order to understand the function of genes and the molecular mechanisms that underlie normal development and disease.

6. **Claim 88** is rejected under 35 U.S.C. 103(a) as being unpatentable by Wallace in view of Ringwald, further in view of Chin, and further in view of Luche et al. (*Pat. No. US 6,649,391, filed on July 19, 2000; hereinafter Luche*).

Regarding **claim 88**, Wallace, as modified by Ringwald and Chin, does not disclose the query result data further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tag data, and pharmacology data.

However, Luche discloses the query result data further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tag data ([Column 29, Lines 50-65), and pharmacology data ([Column 6, Lines 4-6]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Luche with the teachings of

Wallace, as modified by Ringwald and Chin, for the purpose of analyzing sequences in order to provide treatments for various health conditions ([Abstract] of Luche).

7. **Claims 94-98**, **100-108**, **110**, and **112** are rejected under 35 U.S.C. 103(a) as being unpatentable by Wallace in view of Ringwald, further in view of Chin, and further in view of Gibson et al. (*Pub. No. US 2003/0055683, filed on September 19, 2002; hereinafter Gibson*).

Regarding **claim 94**, Wallace clearly shows and discloses a method (*Abstract*) for managing a biological database, comprising:

f. receiving a set of biological sequences (*A set of search query parameters specifying a plurality of sequence sets are received*, [Column 3, Lines 12-14]);

g. querying a plurality of databases with the set of biological sequences (*The structured database query is executed in a database layer. At least one queue handler loading the structured database query is provided. A plurality of biological data repositories are selected*, [Column 3, Lines 32-34]);

h. receiving from the plurality of databases query result data (*Search query parameters are accepted for and search* results displayed from a search request for multiple sequence sets *performed against a plurality of biological data repositories in a user interface layer*, [Column 3, Lines 24-28]) comprising expression data ([Column 3, Lines 32-34]);

i. storing the query result data in a biological database (*The relational database 33 stores tables and queues relating to search requests and results as transacted by the Blast Node 18*, [Column 4, Lines 65-67]), wherein each sequence in the set of biological sequences is associated with a respective record comprising query result data from each of the plurality of databases (*Each biological data repository contains sequence data stored into unstructured records which are each identified by a unique identifier*, [Column 3, Lines 35-40]);

j. periodically performing steps b-d (*if no entries are found (block 234), the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used*, [Column 11, Lines 4-12]);

k. receiving, from a user, a request to view a record of one of the set of biological sequences (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary. The search summary is presented as a table 101 listing out in columns the search name 102, requested user 103, date 104, sequence set 105, databases 106, and deletion flag 107*, [Column 8, Lines 35-45]).

Ringwald then discloses the result data comprising immunohistological data, *in situ* hybridization data (*the Gene Expression Data query provides access to in situ hybridization, and immunohistochmistry data*, [Page 108, Left Column, Paragraph 2]. *Figure 4 further shows query result details for RNA in situ hybridization data*, [Page 110, Figure 4's description]), and structural data comprises three-dimensional structural data

(*3D graphical storage, display, and analysis of in situ expression*, [Page 106, Right Column, Lines 2-6]); and

displaying an executive summary of the record (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace for the purpose of analyzing gene expression in order to understand the function of genes and the molecular mechanisms that underlie normal development and disease.

Chin then discloses the query result data comprising functional data, expression data, wherein functional data comprises data that identifies a putative function, wherein expression data comprises gene expression data or mRNA expression data (*results of a homology search for the plurality of DNA sequences, annotative information for the plurality of DNA sequences describing the biochemical functions and physiological roles of the plurality of DNA sequences, gene expression profile data for the plurality of DNA sequences describing behavioral patterns of the plurality of DNA sequences*, [0011]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Chin with the teachings of Wallace, as modified by Ringwald, for the purpose of facilitating the identification of candidate genes from a plurality of DNA sequences for extracting and integrating information from various information sources and results of various analyses, and

storing the integrated information in a form which is conducive to identification of candidate genes.

Gibson then discloses:

a. providing a plurality of databases (*The PRID system 10 includes client systems 16a, 16b, and 16c. Each client has applications and a local database 17a, 17b, and 17c*, [0024]);

b. determining the version of each of the plurality of databases (*At step 82, the server update process 80 then accesses the appropriate databases to determine if there are updates to the predetermined list of databases*, [0047]);

c. determining if the version of each of the plurality of databases is a current version (*After accessing the predetermined databases, the server update process then determines if there is new data or updates to existing data at step 83*, [0047]);

d. downloading the current version of any of the plurality of databases that is not a current version (*the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database*, [0025]);

e. periodically performing steps b-d (*Periodically, an update file is created for each client with all relevant changes since the last modification of the client database*, [0025]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Gibson with the teachings of Wallace, as modified by Ringwald and Chin, for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of Gibson).

Regarding **claim 95**, Wallace further discloses the plurality of databases comprises two or more databases selected from a group consisting of one or more National Center for Biotechnology Information (NCBI) databases and one or more other externally curated and maintained specialized databases (*Figure 6*).

Regarding **claim 96**, Wallace further discloses periodically performing steps b-d comprises performing steps b-d daily (*the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used*, [Column 11, Lines 4-12]).

Regarding **claim 97**, Wallace further discloses the set of biological sequences comprises a nucleic acid sequence, an amino acid sequence, or a combination thereof (*Figure 4 shows for a new biological data search request, the user enters a search description 71 in a search description text box 72, followed by either a new set of FASTA formatted sequences 73 in a formatted sequence set text box 74, a local file 75 in a local file text box 76, or an existing sequence set 77 in an existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 98**, Wallace further discloses receiving the set of biological sequences comprises receiving the set of biological sequences from a user (*Figure 4 shows for a new biological data search request, the user enters a search description*, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 100**, Wallace further discloses performing one or more bioinformatics functions on the set of biological sequences or the query result data (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]).

Regarding **claim 101**, Wallace further discloses the one or more bioinformatics functions comprise a sequence alignment, a gene identification, a protein identification structure prediction, a motif comparison, a biological text analysis, or a combination thereof (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary. The search summary is presented as a table 101 listing out in columns the search name 102, requested user 103, date 104, sequence set 105, databases 106, and deletion flag 107*, [Column 8, Lines 35-45]).

Regarding **claim 102**, Ringwald further discloses displaying an executive summary of the record comprises formatting the requested record for output to the user (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace, and Chin, for the purpose of analyzing gene expression in order to understand

the function of genes and the molecular mechanisms that underlie normal development and disease.

Regarding **claim 103**, Wallace further discloses a system for managing a biological database (*Figure 1*), comprising:

a target database node, comprising a first memory and a first processor, wherein the first processor is configured to receive and store query result data in the biological database, wherein the biological database comprises a set of biological sequences (*The relational database 33 stores tables and queues relating to search requests and results as transacted by the Blast Node 18*, [Column 4, Lines 65-67]. *A set of search query parameters specifying a plurality of sequence sets are received*, [Column 3, Lines 12-14]) and wherein the query result data comprises comprising expression data ([Column 3, Lines 32-34]); further wherein the target database node is configured to receive, from a user, a request to view a record of one of the set of biological sequences (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]);

a functional node, comprising a third memory and a third processor, wherein the third processor is configured to periodically query the plurality of databases on the query database node with the set of biological sequences from the target database node and send query result data to the target database node (*the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used*, [Column 11, Lines 4-12]); and

a network switch node, comprising a fourth memory and a fourth processor, wherein the fourth processor is configured to direct the receipt and storage of query result data in the biological database, the periodic download and storage of the plurality of databases, and the periodic query of the plurality of databases on the query database node (*Figures 1 and 11*).

Ringwald then discloses the result data comprising immunohistological data, *in situ* hybridization data (*the Gene Expression Data query provides access to in situ hybridization, and immunohistochmistry data*, [Page 108, Left Column, Paragraph 2]. *Figure 4 further shows query result details for RNA in situ hybridization data*, [Page 110, Figure 4's description]), and structural data comprises three-dimensional structural data (*3D graphical storage, display, and analysis of in situ expression*, [Page 106, Right Column, Lines 2-6]); and

displaying an executive summary of the record (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace for the purpose of analyzing gene expression in order to understand the function of genes and the molecular mechanisms that underlie normal development and disease.

Chin then discloses the query result data comprising functional data, expression data, wherein functional data comprises data that identifies a putative function, wherein

expression data comprises gene expression data or mRNA expression data (*results of a homology search for the plurality of DNA sequences, annotative information for the plurality of DNA sequences describing the biochemical functions and physiological roles of the plurality of DNA sequences, gene expression profile data for the plurality of DNA sequences describing behavioral patterns of the plurality of DNA sequences*, [0011]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Chin with the teachings of Wallace, as modified by Ringwald, for the purpose of facilitating the identification of candidate genes from a plurality of DNA sequences for extracting and integrating information from various information sources and results of various analyses, and storing the integrated information in a form which is conducive to identification of candidate genes.

Gibson discloses:

a query node, comprising a second memory and a second processor, wherein the second processor is configured to periodically download and store a plurality of databases from an external network (*Figure 1 shows the PRID system 10 includes client systems 16a, 16b, and 16c. Each client has applications and a local mirror database 17a, 17b, and 17c*, [0024]. *Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database*, [0025]);

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Gibson with the teachings of Wallace, as modified by Ringwald and Chin, for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of Gibson).

Regarding **claim 104**, Wallace further discloses the set of biological sequences comprises a nucleic acid sequence, a amino acid sequence, or a combination thereof (*Figure 4 shows for a new biological data search request, the user enters a search description 71 in a search description text box 72*, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 105**, Wallace further discloses the functional node is further configured to perform one or more bioinformatics functions on the set of biological sequences or the query result data and update the target database node (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]).

Regarding **claim 106**, Wallace further discloses the one or more bioinformatics functions comprise a sequence alignment, a gene identification, a protein identification structure prediction, a motif comparison, and a biological text analysis, or a combination thereof (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary*, [Column 8, Lines 35-45]).

Regarding **claim 107**, Wallace further discloses the plurality of databases comprises two or more databases selected from a group consisting of one ore more National Center for Biotechnology Information (NCBI) databases and one or more other externally curated and maintained specialized databases (*Figure 6*).

Regarding **claim 108**, Wallace further discloses the query node is further configured to periodically download and store a plurality of databases from an external network daily (*the Blast node 53 sleeps for a pre-determined interval (block 235). In the described embodiment, an interval of 2,000 milliseconds is used, although other suitable intervals could also be used*, [Column 11, Lines 4-12]).

Regarding **claim 110**, Wallace further discloses each of sequences in the set of biological sequences is associated with a record comprising query result data from each of the plurality of databases (*Each biological data repository contains sequence data stored into unstructured records which are each identified by a unique identifier. The structured database query is executed against at least one database engine. The database results are obtained from the selected biological data repositories*, [Column 3, Lines 35-40]).

Regarding **claim 112**, Ringwald further discloses the target database node is further configured to format the requested record for output to the user (*Figure 4 shows displaying an analysis of an expression record for in situ data*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Ringwald with the teachings of Wallace, Chin, and Gibson, for the purpose of analyzing gene expression in order to

understand the function of genes and the molecular mechanisms that underlie normal development and disease.

8. **Claims 99**, and **109** are rejected under 35 U.S.C. 103(a) as being unpatentable by Wallace in view of Ringwald, in view of Chin, and further in view of Gibson, and further in view of Luche.

Regarding **claims 99**, and **109**, Wallace, as modified by Ringwald, Chin and Gibson, does not disclose the query result data further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tag data, and pharmacology data.

However, Luche discloses the query result data further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tag data ([Column 29, Lines 50-65), and pharmacology data ([Column 6, Lines 4-6]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Luche with the teachings of Wallace, as modified by Ringwald, Chin, and Gibson, for the purpose of analyzing sequences in order to provide treatments for various health conditions ([Abstract] of Luche).

Conclusion

9. These following prior arts made of record and not relied upon are considered pertinent to Applicant's disclosure:

Weidl et al. (*Pub. No. US 2005/0015217*) teaches analyzing events to diagnose symptoms and causes of a root problem.

Ohsuga (*Pat. No. US 6,171,109*) teaches method for generating a multistrata model and intellectual information processing device.

Contact Information

10. Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Son T. Hoang whose telephone number is (571) 270-1752. The Examiner can normally be reached on Monday – Friday (7:00 AM – 4:00 PM).

If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Neveen Abel-Jalil can be reached on (571) 272-4074. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO

Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Son T Hoang/
Examiner, Art Unit 2165
December 17, 2010